

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

22. (Currently Amended) A method of generating from a sample a high-resolution protein expression fingerprint dataset containing a plurality of polypeptide sequence tags, comprising:

(i) obtaining a protein-containing extract from said sample, wherein said sample comprises a plurality of intact proteins;

(ii) electrophoresing said extract in a multidimensional capillary electrophoresis device having an electroosmotic flow of less than 1×10^{-4} cm²/V-s to separate and elute intact protein species to resolve said intact protein species based on at least one first biophysical parameter which discriminates protein species;

(iii) obtaining, by mass spectrographic fragmentation of a plurality of eluted intact protein species, a plurality of polypeptide sequence tags; **and**

(iv) generating a high-resolution protein expression fingerprint dataset containing said plurality of polypeptide sequence tags.

23. (Previously Presented) The method of claim 1, wherein the method further comprises, prior to step (iii):

(iia) electrophoresing eluted intact protein species eluted from said multidimensional capillary electrophoresis device in a second capillary electrophoresis device, or plurality thereof in parallel, to separate and elute intact protein species thereby resolving said protein species based on at least one second biophysical parameter which discriminates protein species.

24. (Previously Presented) The method of claim 22, further comprising quantitating said plurality of eluted intact protein species, thereby including the relative abundance of said plurality of eluted intact protein species in said high-resolution protein expression fingerprint dataset.

25. (Previously Presented) The method of claim 22, further comprising storing said high-resolution protein expression fingerprint dataset in computer-retrievable form.

26. (Previously Presented) The method of claim 22, wherein said plurality of eluted intact protein species is at least 100 eluted intact protein species.

27. (Previously Presented) The method of claim 26, further comprising quantitating said at least 100 eluted intact protein species, thereby including the relative abundance of said at least 100 eluted intact protein species in said high-resolution protein expression fingerprint dataset.

28. (Previously Presented) The method of claim 22, further comprising determining the separation coordinates of said plurality of eluted intact protein species, thereby including the separation coordinates of said plurality of eluted intact protein species in said high-resolution protein expression fingerprint dataset.

29. (Previously Presented) The method of claim 22, wherein said sample is a tissue sample known to be free of pathological disorders.

30. (Previously Presented) The method of claim 22, wherein said sample is a tissue sample known to contain at least one pathological disorder.